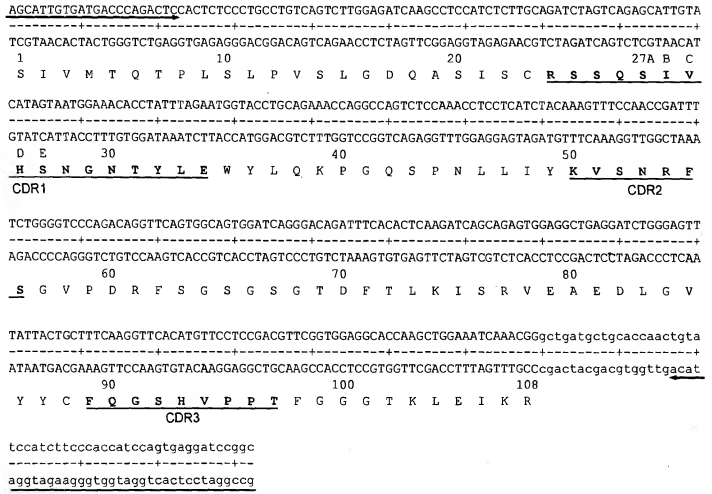

Figure 1A shows the DNA sequence encoding MN3Vk cloned by RT-PCR and the predicted amino acid sequence. Underlined arrows indicate the PCR primer sequences. The putative CDR regions are in bold and underlined, and indicated. Nucleotide residues are numbered sequentially (right side). Kabat's Ig molecule numbering is used for amino acid residues (top of the residues).

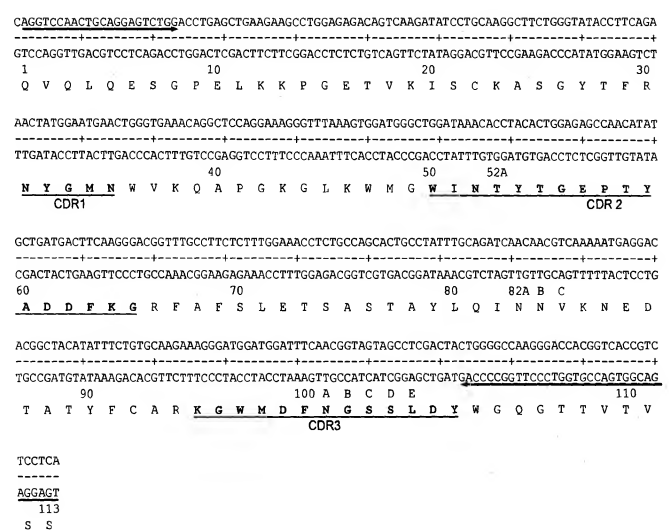

Figure 1B shows the DNA sequence encoding MN3VH cloned by RT-PCR and the predicted amino acid sequence. Underlined arrows indicate the PCR primer sequences. The putative CDR regions are in bold and underlined, and indicated. Nucleotide residues are numbered sequentially (right side). Kabat's Ig molecule numbering is used for amino acid residues (top of the residues).

```
GACATCCAGCTGACCCAGACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCCATCTCTTGCAGATCTAGTCAGAGCATTGTA
---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+  90
CTGTAGGTCGACTGGGTCTGAGGTGAGAGGGACGGACAGTCAGAACCTCTAGTTCGGAGGTAGAGAACGTCTAGATCAGTCTCGTAACAT

 D  I  Q  L  T  Q  T  P  L  S  L  P  V  S  L  G  D  Q  A  S  I  S  C  R  S  S  Q  S  I  V     30


CATAGTAATGGAAACACCTATTTAGAATGGTACCTGCAGAAACCAGGCCAGTCTCCAAACCTCCTCATCTACAAAGTTTCCAACCGATTT
---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 180
GTATCATTACCTTTGTGGATAAATCTTACCATGGACGTCTTTGGTCCGGTCAGAGGTTTGGAGGAGTAGATGTTTCAAAGGTTGGCTAAA

 H  S  N  G  N  T  Y  L  E  W  Y  L  Q  K  P  G  Q  S  P  N  L  L  I  Y  K  V  S  N  R  F     55
CDR1                                                                          CDR2
TCTGGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTT
---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 270
AGACCCCAGGGTCTGTCCAAGTCACCGTCACCTAGTCCCTGTCTAAAGTGTGAGTTCTAGTCGTCTCACCTCCGACTCCTAGACCCTCAA

 S  G  V  P  D  R  F  S  G  S  G  S  G  T  D  F  T  L  K  I  S  R  V  E  A  E  D  L  G  V     85


TATTACTGCTTTCAAGGTTCACATGTTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAGATCAAACGT
---------+---------+---------+---------+---------+---------+---------+---------+---------       339
ATAATGACGAAAGTTCCAAGTGTACAAGGAGGCTGCAAGCCACCTCCGTGGTTCGACCTCTAGTTTGCA

 Y  Y  C  F  Q  G  S  H  V  P  P  T  F  G  G  G  T  K  L  E  I  K  R                          108
             CDR3
```

Figure 2A shows the DNA and amino acid sequences of cMN3Vk domain. The CDR regions are in bold, underlined, and indicated. Nucleotide residues are numbered sequentially. Kabat's Ig molecule numbering is used for amino acid residues (same as in Fig. 1A).

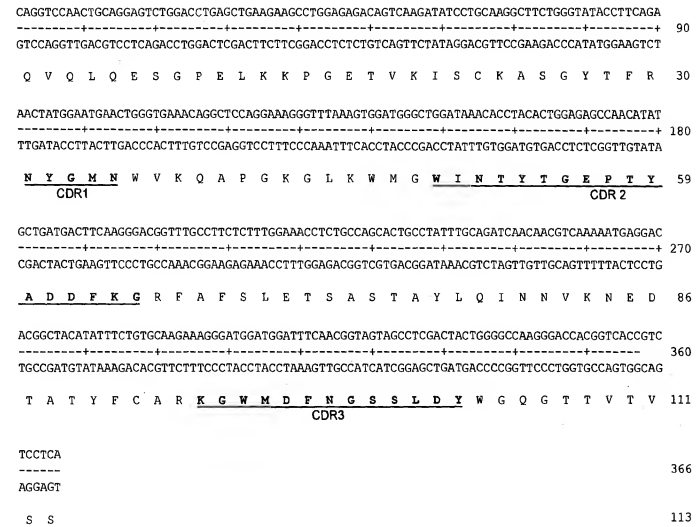

Figure 2B shows the DNA and amino acid sequences of cMN3VH domain. The CDR regions are in bold, underlined, and indicated. Nucleotide residues are numbered sequentially. Kabat's Ig molecule numbering is used for amino acid residues (same as in Fig. 1B).

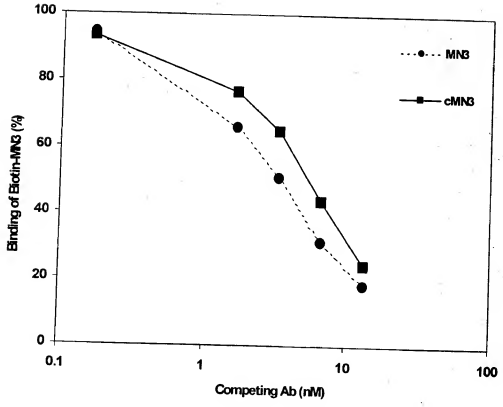
100
80
60
40
20
0
Binding of Biotin-MN3 (%)
0.1
1
10
100
Competing Ab (nM)
MN3
cMN3

Figure 3.

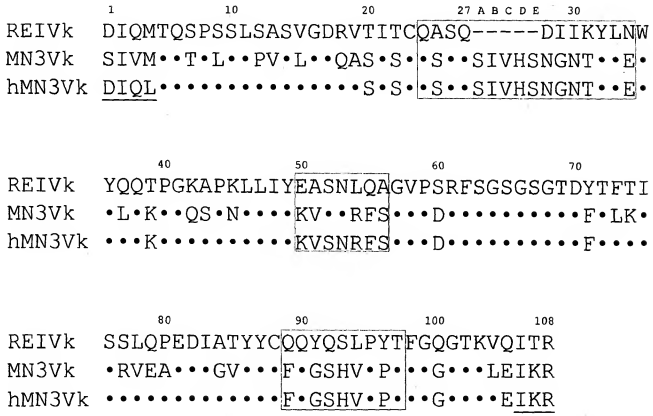

Figure 4A. Amino acid sequence alignment of REI, MN3 and hMN3 light chain variable domains. Dots indicate the residues in MN3 is identical to the corresponding residues in REI. Dashes represent gaps introduced to aid the alignment. Boxed represent the CDR regions. Both N- and C-terminal residues (underlined) of hMN3 are fixed by the staging vector used. Therefore, the corresponding terminal residues of MN3 are not compared with that of REI. Kabat's Ig molecule numbering scheme is used (same as in Fig. 1A).

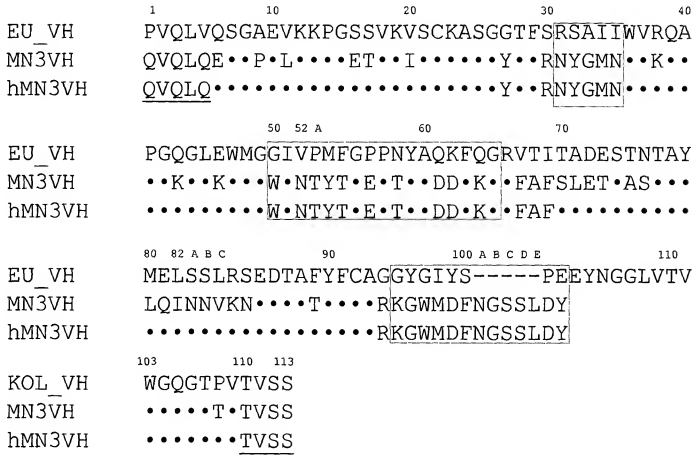

Figure4B. Amino acid sequence alignment of EU (FR1-3) and KOL (FR4), MN3 and hMN3 heavy chain variable domains. Dots indicate the residues in MN3 is identical to the corresponding residues in REI. Dashes represent gaps introduced to aid the alignment. Boxed represent the CDR regions. Both N- and C-terminal residues (underlined) of hMN3 are fixed by the staging vector used. Therefore, the corresponding terminal residues of MN3 are not compared with that of human VH sequences. Kabat's Ig molecule numbering scheme is used (same as in Fig. 1A).

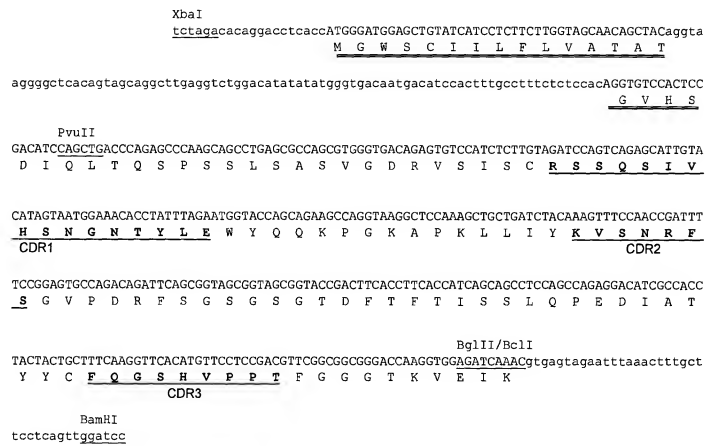

Figure 5A.

Title: CHIMERIC, HUMAN AND HUMANIZED ANTI-GRANULOCYTE ANTIBODIES AND METHODS OF USE
Inventor(s): GOLDENBERG et al.
Atty. Dkt. No.: 018733-1267

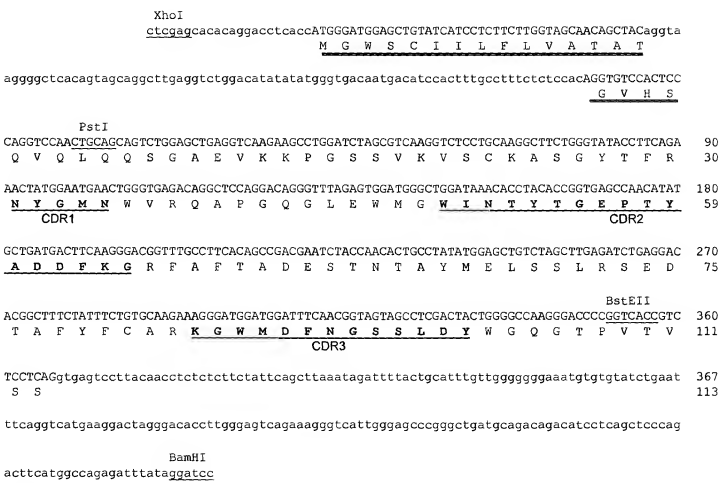
XhoI
ctcgagcacacaggacctcaccATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACaggta
M G W S C I I L F L V A T A T
agggggctcacagtagcaggcttgaggtctggacatatatatgggtgacaatgacatccactttgccttttctctccacAGGTGTCCACTCC
G V H S
PstI
CAGGTCCAACTGCAGCAGTCTGGAGCTGAGGTCAAGAAGCCTGGATCTAGCGTCAAGGTCTCCTGCAAGGCTTCTGGGTATACCTTCAGA 90
Q V Q L Q Q S G A E V K K P G S S V K V S C K A S G Y T F R 30
AACTATGGAATGAACTGGGTGAGACAGGCTCCAGGACAGGGTTTAGAGTGGATGGGCTGGATAAACACCTACACCGGTGAGCCAACATAT 180
N Y G M N W V R Q A P G Q G L E W M G W I N T Y T G E P T Y 59
CDR1
CDR2
GCTGATGACTTCAAGGGACGGTTTGCCTTCACAGCCGACGAATCTACCAACACTGCCTATATGGAGCTGTCTAGCTTGAGATCTGAGGAC 270
A D D F K G R F A F T A D E S T N T A Y M E L S S L R S E D 75
BstEII
ACGGCTTTCTATTTCTGTGCAAGAAAGGGATGGATGGATTTCAACGGTAGTAGCCTCGACTACTGGGGCCAAGGGACCCCGGTCACCGTC 360
T A F Y F C A R K G W M D F N G S S L D Y W G Q G T P V T V 111
CDR3
TCCTCAGgtgagtccttacaacctctctcttctattcagcttaaatagattttactgcatttgttgggggggaaatgtgtgtatctgaat 367
S S 113
ttcaggtcatgaaggactagggacaccttgggagtcagaaagggtcattgggagcccgggctgatgcagacagacatcctcagctcccag
BamHI
acttcatggccagagatttataggatcc

Figure 5B.

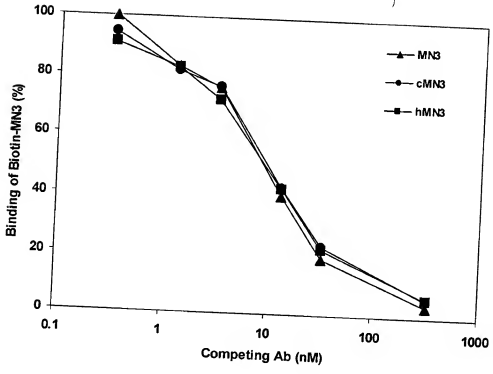
100
80
60
40
20
0
Binding of Biotin-MN3 (%)
0.1
1
10
100
1000
Competing Ab (nM)
MN3
cMN3
hMN3

Figure 6.